



SEQUENCE LISTING

<110> Barnett, Susan
Zur Megede, Jan

<120> POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

<130> 1631.002

<140> 09/475,704

<141> 1999-12-30

<150> 60/152,195

<151> 1999-09-01

<160> 30

<170> PatentIn Ver. 2.0

<210> 1

<211> 60

<212> DNA

<213> Human immunodeficiency virus

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<210> 2

<211> 60

<212> DNA

<213> Human immunodeficiency virus

<400> 2

gacatccgcc agggcccaaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 60

<210> 3

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110965

<400> 3

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ctggagaagt tcgccctgaa ccccggcctg ctggagacca gcgagggctg caagcagatc 180
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accgtggcca ccctgtactg cgtgcacgag aagatcgagg tccgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaaggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggatgat cgaggagaag 480

gccttcagcc ccgaggtgat ccccatgttc accgccttga gcgagggcgc cccccccag 540
gacctgaaca cgatgttgaa caccgtgggc ggccaccagg ccgcatgca gatgctgaag 600

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ctgcaggagc	agatcgccctg	gatgaccagc	aaccccccca	tccccgtggg	cgacatctac	780
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ttcgaggaga	ccaccccccg	ccagaagcag	gagagcaagg	accgcgagac	cctgaccagc	1440
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<210> 4

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
of HIV strain AF110967

<400> 4

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accgtggcca	ccctgtactg	cgtgcacgcc	ggcatcgagg	tccgcgacac	caaggaggcc	300
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gccgacggca	aggtgagcca	gaactacccc	atcgtgcaga	acctgcaggg	ccagatgggtg	420
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cccggcaact	tcctgcagaa	ccgcagcgag	ccgcgcgccc	ccaccgtgcc	caccgcccc	1380
cccgcgaga	gcttccgctt	cgaggagacc	acccccgccc	ccaagcagga	gcccaggac	1440
cgcgagccct	accgcgagcc	cctgaccgcc	ctgcgcagcc	tgttcggcag	cggccccctg	1500
agccagtaa						1509

<210> 5

<211> 141

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Env common
region of HIV strain AF110968

<400> 5

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gccatgtacg ccccccccat cgccggcaac ctgacctgcg agagcaacat caccggcctg 120
ctgctgaccc gcgacggcgg c                                     141
```

<210> 6

<211> 1431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110968

<400> 6

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aagaccaccc tgttctgcac cagcgacgcc aaggcctacg agaccgaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccaccgac cccaaccccc aggagatcgt gctggagaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc tgcgtgaagc tgacccccct gtgctgacc 300
ctgaagtgcc gcaacgtgaa cgccaccaac aacatcaaca gcatgatcga caacagcaac 360
aagggcgaga tgaagaactg cagcttcaac gtgaccaccg agctgcgcga ccgcaagcag 420
gaggtgcacg cctgtttcta ccgcctggac gtggtgcccc tgcagggcaa caacagcaac 480
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ttcgacccca tccccatcca ctactgcacc ccgcctggct acgccatcct gaagtgcaac 600
aaccagacct tcaacggcac cggccccctgc aacaacgtga gcagcgtgca gtgcgccccac 660
ggcatcaagc ccgtggtgag caccagctg ctgctgaacg gcagcctggc caagggcgag 720
atcatcatcc gcagcgagaa cctggccaac aacgccaaga tcatcatcgt gcagctgaac 780
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ggcgtggccc ccaccgaggc caagcgccgc gtggtggagc gcgagaagcg c 1431
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<210> 7

<211> 1944

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110968

<400> 7

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gtgaccgaga	acttcaacat	gtggaagaac	gacatggtgg	accagatgca	cgaggacatc	240
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atcaacaact	acaccgacac	catctaccgc	ctgctggagg	agagccagaa	ccagcaggag	1860
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<210> 8

<211> 2466

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110968

<400> 8

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tggggccaccc	acgcctgcgt	gcccaccgac	cccaaccccc	aggagatcgt	gctggagaac	180
gtgaccgaga	acttcaacat	gtggaagaac	gacatggtgg	accagatgca	cgaggacatc	240
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ctgaagtgcc	gcaacgtgaa	cgccaccaac	aacatcaaca	gcatgatcga	caacagcaac	360
aagggcgaga	tgaagaactg	cagcttcaac	gtgaccaccg	agctgcgcga	ccgcaagcag	420
gaggtgcacg	ccctgttcta	ccgcctggac	gtggtgcccc	tgacgggcaa	caacagcaac	480
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ttcgacccca	tccccatcca	ctactgcacc	cccgcggct	acgccatcct	gaagtgcaac	600
aaccagacct	tcaacggcac	cggccccctgc	aacaacgtga	gcagcgtgca	gtgcgcccac	660
ggcatcaagc	ccgtggtgag	caccagctg	ctgctgaacg	gcagcctggc	caagggcgag	720
atcatcatcc	gcagcgagaa	cctggccaac	aacgccaaga	tcatcatcgt	gcagctgaac	780

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<210> 9

<211> 2547

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110968

<400> 9

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gtgcccgtgt ggaaggaggc caagaccacc ctgttctgca ccagcgacgc caaggcctac 180
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gaccagatgc acgaggacat catcagcctg tgggaccaga gcctgaagcc ctgcgtgaag 360
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gaccgcctgg	gccgcctcga	ggaggagggg	ggcgagcagg	accgcggccg	cagcatccgc	2220
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<210> 10

<211> 1035

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic a
gp41 coding region of HIV strain AF110968

<400> 10

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gccctgaagt	acctgggcag	cctggtgcag	tactggggcc	tggagctgaa	gaagagcgcc	900
atcagcctgc	tggacaccat	cgccatcgcc	gtggccgagg	gcaccgaccg	catcatcgag	960
ttcatccagc	gcacatgccg	cgccatccgc	aacatcccc	gccgcacccg	ccagggttc	1020

gaggccgccc tgcag

1035

<210> 11

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Env
common region of HIV strain AF110975

<400> 11

agcatcatca ccctgccctg ccgcatcaag cagatcatcg acatgtggca gaaggtgggc 60
cgcgccatct acgccccccc catcgagggc aacatcacct gcagcagcag catcaccggc 120
ctgctgctgg cccgcgacgg cggc 144

<210> 12

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp120 coding region of HIV strain AF110975

<400> 12

agcggcctgg gcaacctgtg ggtgaccgtg tacgacggcg tgcccgtgtg gcgcgaggcc 60
agcaccaccc tgttctgcgc cagcgacgcc aaggcctacg agaaggaggt gcacaacgtg 120
tgggccaccc acgcctgcgt gccacccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
atcagcctgt gggaccagag cctgaagccc cgcgtgaagc tgacccccct gtgctgacc 300
ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgcccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaaag 540
gtgagcttcg accccatccc catccactac tgcgcccccg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccctgccaga acgtgagcac cgtgcagtgc 660
accacggca tcaagcccgt ggtgagcacc ccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
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ggcgacatga aggacaactg gcgcaacgag ctgtacaagt acaaggtggt ggagatcaag 1380
cccctgggcg tggccccac cgaggccaag cgccgcgtgg tggagcgcgga gaagcgc 1437

<210> 13

<211> 1950

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp140 coding region of HIV strain AF110975

<400> 13

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tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
gtgaccgaga acttcaacat gtggaagaac gacatggtgg accagatgca cgaggacatc 240
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ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
aagaagcagc aggtgtacgc cctgttctac aagctggaca tcgtgccccct gaacagcaac 480
agcagcgagt accgcctgat caactgcaac accagcgcca tcaccaggc ctgccccaa 540
gtgagcttcg accccatccc catccactac tgcccccgcg ccggctacgc catcctgaag 600
tgcaagaaca acaccagcaa cggcaccggc ccttgccaga acgtgagcac cgtgcagtgc 660
acccacggca tcaagcccgt ggtgagcacc cccctgctgc tgaacggcag cctggccgag 720
ggcggcgaga tcatcatccg cagcaagaac ctgagcaaca acgcctacac catcatcgtg 780
cacctgaacg acagcgtgga gatcgtgtgc acccgcccca acaacaacac ccgcaagggc 840
atccgcatcg gccccggcca gaccttctac gccaccgaga acatcatcgg cgacatccgc 900
caggcccaact gcaacatcag cgccggcgag tggaacaagg ccgtgcagcg cgtgagcgcc 960
aagctgcgcg agcacttccc caacaagacc atcgagttcc agcccagcag cggcggcgac 1020
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aagctgttca acagcagcta caacggcacc agctaccgcg gcaccgagag caacagcagc 1140
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ttcaacatca gcaactggct gtggtacatc 1950
```

<210> 14

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
gp160 coding region of HIV strain AF110975

<400> 14

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tgggccaccc acgcctgcgt gcccaccgac cccaaccccc aggagatcga gctggacaac 180
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ctgaagtgca ccaactacag caccaactac agcaacacca tgaacgccac cagctacaac 360
aacaacacca ccgaggagat caagaactgc accttcaaca tgaccaccga gctgcgcgac 420
```


aagaagcagc	aggtgtacgc	cctgttctac	aagctggaca	tcgtgcccct	gaacagcaac	480
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gtgagcttcg	accccatccc	catccactac	tgcgcccccg	ccggctacgc	catcctgaag	600
tgcaagaaca	acaccagcaa	cggcaccggc	ccctgccaga	acgtgagcac	cgtgcagtgc	660
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accgaccgca	tcatcgaggt	gatccagcgc	atctaccgcg	ccttctgcaa	catccccgcg	2460
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<210> 15

<211> 2565

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence and gp160 coding region of HIV
strain AF110975

<400> 15

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ttctggatct	gcagcggcct	gggcaacctg	tgggtgaccg	tgtacgacgg	cgtgcccgtg	120
tggcgcgagg	ccagcaccac	cctgttctgc	gccagcgacg	ccaaggccta	cgagaaggag	180
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cacgaggaca	tcatcagcct	gtgggaccag	agcctgaagc	cccgcgtgaa	gctgaccccc	360
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accagctaca	acaacaacac	caccgaggag	atcaagaact	gcaccttcaa	catgaccacc	480
gagctgcgcg	acaagaagca	gcagggtgtac	gccctgttct	acaagctgga	catcgtgccc	540

ctgaacagca	acagcagcga	gtaccgcctg	atcaactgca	acaccagcgc	catcacccag	600
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<210> 16

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic a
gp41 coding region of HIV strain AF110975

<400> 16

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cagagcaacc	tgctgcgcgc	catcgaggcc	cagcagcaca	tgctgcagct	gaccgtgtgg	180
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agcagctgga	gcaacaagac	ccaggggcag	atctgggaga	acatgacctg	gatgcagtgg	360
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tggttcaaca	tcagcaactg	gctgtggtac	atcaagatct	tcattcatgat	cgtggggcggc	540
ctgatecgcc	tgcgcattcat	cttcgccgtg	ctgagcatcg	tgaaccgcgt	gcgccagggc	600
tacagcccc	tgagcttcca	gacctgacc	cccaaccccc	gcggcctgga	ccgcctgggc	660

cgcacgcagg aggagggcgg cgagcaggac cgcgaccgca gcatccgcct ggtgcagggc 720
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<210> 17

<211> 492

<212> PRT

<213> Human immunodeficiency virus

<400> 17

Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Gly Lys Leu Asp Ala Trp
 1 5 10 15

Glu Arg Ile Arg Leu Arg Pro Gly Gly Lys Lys Cys Tyr Met Met Lys
 20 25 30

His Leu Val Trp Ala Ser Arg Glu Leu Glu Lys Phe Ala Leu Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Ile Arg Gln Leu
 50 55 60

His Pro Ala Leu Gln Thr Gly Ser Glu Glu Leu Lys Ser Leu Phe Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
 100 105 110

Gln Lys Ile Gln Gln Ala Glu Ala Ala Asp Lys Gly Lys Val Ser Gln
 115 120 125

Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala
 130 135 140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys
 145 150 155 160

Ala Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly
 165 170 175

Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His
 180 185 190

Gln Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala
 195 200 205

Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly
 210 215 220

Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr

225		230		235		240
Leu Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val						
		245		250		255
Gly Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val						
		260		265		270
Arg Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Lys Gln Gly Pro Lys						
		275		280		285
Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala						
		290		295		300
Glu Gln Ser Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu						
		305		310		315
Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly						
		325		330		335
Pro Gly Ala Ser Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly						
		340		345		350
Gly Pro Ser His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Ala						
		355		360		365
Asn Thr Ser Val Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg						
		370		375		380
Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn						
		385		390		395
						400
Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly						
		405		410		415
His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys						
		420		425		430
Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Ser Arg						
		435		440		445
Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr						
		450		455		460
Thr Pro Gly Gln Lys Gln Glu Ser Lys Asp Arg Glu Thr Leu Thr Ser						
		465		470		475
						480
Leu Lys Ser Leu Phe Gly Asn Asp Pro Leu Ser Gln						
		485		490		

<210> 18

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110968

<400> 18

atgcgcgtga tgggcatcct gaagaactac cagcagtggg ggatgtgggg catcctgggc 60
ttctggatgc tgatcatcag c 81

<210> 19

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic
signal sequence of HIV strain AF110975

<400> 19

atgcgcgtgc gcggcatcct gcgcagctgg cagcagtggg ggatctgggg catcctgggc 60
ttctggatct gc 72

<210> 20

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic Gag
coding sequence of HIV strain AF110965

<400> 20

atgggcgccc gcgccagcat cctgcgcggc ggcaagctgg acgcctggga gcgcatccgc 60
ctgcgccccg gcggcaagaa gtgctacatg atgaagcacc tgggtgtggg cagccgcgag 120
ctggagaagt tcgccctgaa ccccgccctg ctggagacca gcgagggctg caagcagatc 180
atccgcccagc tgcaccccgc cctgcagacc ggcagcagagg agctgaagag cctgttcaac 240
accgtggcca cctgtactg cgtgcacgag aagatcgagg tgcgcgacac caaggaggcc 300
ctggacaaga tcgaggagga gcagaacaag tgccagcaga agatccagca ggccgaggcc 360
gccgacaagg gcaagggtgag ccagaactac cccatcgtgc agaacctgca gggccagatg 420
gtgcaccagg ccatcagccc ccgcaccctg aacgcctggg tgaaggatgat cgaggagaag 480
gccttcagcc ccgagggtgat ccccatgttc accgccttga gcgagggcgc cccccccag 540
gacctgaaca ccatgctgaa caccgtgggc ggccaccagg ccgccatgca gatgctgaag 600
gacaccatca acgaggaggc cgccgagtgg gaccgcgtgc acccctgca cgccggcccc 660
atcgcccccg gccagatgag cgagccccgc ggcagcagaca tcgccggcac caccagcacc 720
ctgcaggagc agatcgctg gatgaccagc aaccccccca tccccgtggg cgacatctac 780
aagcgctgga tcatcctggg cctgaacaag atcgtgcgca tgtacagccc cgtgagcatc 840
ctggacatca agcaggggccc caaggaggccc ttccgcgact acgtggaccg cttcttcaag 900
accctgcgcg ccgagcagag caccagagg gtgaagaact ggatgaccga caccctgctg 960
gtgcagaacg ccaaccccga ctgcaagacc atcctgcgcg ccctggggccc cgccgcccagc 1020
ctggaggaga tgatgaccgc ctgccagggc gtgggcccgg ccagccacaa ggcccgcgtg 1080
ctggccgagg ccatgagcca ggccaacacc agcgtgatga tgcagaagag caacttcaag 1140
ggcccccgcc gcatcgtgaa gtgcttcaac tgcggcaagg agggccacat cgcccgcac 1200
tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
gactgcaccg agcgcaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
cccggcaact tctgcagag ccgccccgag cccaccgccc ccccgccga gagcttccgc 1380
ttcgaggaga ccacccccgg ccagaagcag gagagcaagg accgcgagac cctgaccagc 1440
ctgaagagcc tgttcggcaa cgaccccctg agccagtaa 1479

<210> 21
 <211> 1509
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: synthetic Gag
 coding sequence of HIV strain AF110967

<400> 21
 atgggcgccc gcgccagcat cctgcgcggc gagaagctgg acaagtggga gaagatccgc 60
 ctgcgccccg gcggcaagaa gcactacatg ctgaagcacc tgggtgtggg cagccgcgag 120
 ctggaggggt tcgccctgaa ccccggcctg ctggagaccg ccgagggctg caagcagatc 180
 atgaagcagc tgcagcccgc cctgcagacc ggcaccgagg agctgcgcag cctgtacaac 240
 accgtggcca ccctgtactg cgtgcacgcc ggcacgcagg tgcgcgacac caaggaggcc 300
 ctggacaaga tcgaggagga gcagaacaag agccagcaga agaccagca ggccaaggag 360
 gccgacggca aggtgagcca gaactacccc atcgtgcaga acctgcaggg ccagatggtg 420
 caccaggcca tcagcccccg caccctgaac gcctgggtga aggtgatcga ggagaaggcc 480
 ttcagccccg aggtgatccc catgttcacc gccctgagcg agggcgccac ccccaggac 540
 ctgaacacca tgctgaacac cgtgggcggc caccaggccg ccattgcagat gctgaaggac 600
 accatcaacg aggaggccgc cgagtgggac cgcctgcacc ccgtgcaggc cggccccgtg 660
 gccccgggcc agatgcgcga ccccgcgggc agcgacatcg ccggcgccac cagcaccctg 720
 caggagcaga tcgcctggat gaccagcaac cccccgtgc ccgtgggcga catctacaag 780
 cgctggatca tcctgggcct gaacaagatc gtgcgcgatg acagccccgt gagcatcctg 840
 gacatccgcc agggccccaa ggagcccttc cgcgactacg tggaccgctt cttcaagacc 900
 ctgcgcgccc agcaggccac ccaggacgtg aagaactgga tgaccgagac cctgctggtg 960
 cagaacgcc accccgactg caagaccatc ctgcgcgccc tgggcccccg cgccaccctg 1020

 gaggagatga tgaccgcctg ccaggggcgtg ggcgcccccg gccacaaggc ccgcgtgctg 1080
 gccgaggcca tgagccaggc caacagcgtg aacatcatga tgcagaagag caacttcaag 1140
 ggcccccgcc gcaacgtgaa gtgcttcaac tgcggcaagg agggccacat cgccaagaac 1200
 tgccgcgccc cccgcaagaa gggctgctgg aagtgcggca aggagggcca ccagatgaag 1260
 gactgcaccg agcgccaggc caacttcctg ggcaagatct ggcccagcca caagggccgc 1320
 cccggcaact tcctgcagaa ccgcagcgag cccgcgcgcc ccaccgtgcc caccgcccc 1380
 cccgcgcgaga gcttccgctt cgaggagacc acccccgccc ccaagcagga gcccaaggac 1440
 cgcgagccct accgcgagcc cctgaccgcc ctgcgcagcc tgttcggcag cggccccctg 1500
 agccagtaa 1509

<210> 22
 <211> 502
 <212> PRT
 <213> Human immunodeficiency virus

<400> 22
 Met Gly Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1 5 10 15

 Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
 20 25 30

 His Leu Val Trp Ala Ser Arg Glu Leu Glu Gly Phe Ala Leu Asn Pro
 35 40 45

 Gly Leu Leu Glu Thr Ala Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
 50 55 60

Gln	Pro	Ala	Leu	Gln	Thr	Gly	Thr	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn	
65					70					75					80	
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Ala	Gly	Ile	Glu	Val	Arg	Asp	
				85					90					95		
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Gln	
			100					105					110			
Gln	Lys	Thr	Gln	Gln	Ala	Lys	Glu	Ala	Asp	Gly	Lys	Val	Ser	Gln	Asn	
		115					120					125				
Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	Gln	Ala	Ile	
	130					135					140					
Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Ile	Glu	Glu	Lys	Ala	
145					150					155					160	
Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Thr	Ala	Leu	Ser	Glu	Gly	Ala	
				165					170					175		
Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	
			180					185					190			
Ala	Ala	Met	Gln	Met	Leu	Lys	Asp	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	
		195					200					205				
Trp	Asp	Arg	Leu	His	Pro	Val	Gln	Ala	Gly	Pro	Val	Ala	Pro	Gly	Gln	
	210					215					220					
Met	Arg	Asp	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Ala	Thr	Ser	Thr	Leu	
225					230					235					240	
Gln	Glu	Gln	Ile	Ala	Trp	Met	Thr	Ser	Asn	Pro	Pro	Val	Pro	Val	Gly	
				245					250					255		
Asp	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg	
			260					265					270			
Met	Tyr	Ser	Pro	Val	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu	
		275					280					285				
Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Phe	Lys	Thr	Leu	Arg	Ala	Glu	
	290					295					300					
Gln	Ala	Thr	Gln	Asp	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val	
305					310					315					320	
Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Arg	Ala	Leu	Gly	Pro	
				325					330					335		
Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly	
			340					345					350			
Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	Gln	Ala	Asn	
		355					360					365				

Ser Val Asn Ile Met Met Gln Lys Ser Asn Phe Lys Gly Pro Arg Arg
 370 375 380
 Asn Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Lys Asn
 385 390 395 400
 Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
 405 410 415
 His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
 420 425 430
 Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
 435 440 445
 Ser Glu Pro Ala Ala Pro Thr Val Pro Thr Ala Pro Pro Ala Glu Ser
 450 455 460
 Phe Arg Phe Glu Glu Thr Thr Pro Ala Pro Lys Gln Glu Pro Lys Asp
 465 470 475 480
 Arg Glu Pro Tyr Arg Glu Pro Leu Thr Ala Leu Arg Ser Leu Phe Gly
 485 490 495
 Ser Gly Pro Leu Ser Gln
 500

<210> 23
 <211> 849
 <212> PRT
 <213> Human immunodeficiency virus

<400> 23
 Met Arg Val Met Gly Ile Leu Lys Asn Tyr Gln Gln Trp Trp Met Trp
 1 5 10 15
 Gly Ile Leu Gly Phe Trp Met Leu Ile Ile Ser Ser Val Val Gly Asn
 20 25 30
 Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Lys
 35 40 45
 Thr Thr Leu Phe Cys Thr Ser Asp Ala Lys Ala Tyr Glu Thr Glu Val
 50 55 60
 His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
 65 70 75 80
 Gln Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met Trp Lys
 85 90 95
 Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
 100 105 110
 Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu

115					120					125					
Lys	Cys	Arg	Asn	Val	Asn	Ala	Thr	Asn	Asn	Ile	Asn	Ser	Met	Ile	Asp
130					135					140					
Asn	Ser	Asn	Lys	Gly	Glu	Met	Lys	Asn	Cys	Ser	Phe	Asn	Val	Thr	Thr
145					150					155					160
Glu	Leu	Arg	Asp	Arg	Lys	Gln	Glu	Val	His	Ala	Leu	Phe	Tyr	Arg	Leu
				165					170					175	
Asp	Val	Val	Pro	Leu	Gln	Gly	Asn	Asn	Ser	Asn	Glu	Tyr	Arg	Leu	Ile
			180					185					190		
Asn	Cys	Asn	Thr	Ser	Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe
		195					200					205			
Asp	Pro	Ile	Pro	Ile	His	Tyr	Cys	Thr	Pro	Ala	Gly	Tyr	Ala	Ile	Leu
	210					215					220				
Lys	Cys	Asn	Asn	Gln	Thr	Phe	Asn	Gly	Thr	Gly	Pro	Cys	Asn	Asn	Val
225					230					235					240
Ser	Ser	Val	Gln	Cys	Ala	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Gln
				245					250					255	
Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Lys	Gly	Glu	Ile	Ile	Ile	Arg	Ser
			260					265					270		
Glu	Asn	Leu	Ala	Asn	Asn	Ala	Lys	Ile	Ile	Ile	Val	Gln	Leu	Asn	Lys
		275					280					285			
Pro	Val	Lys	Ile	Val	Cys	Val	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Ser
		290				295					300				
Val	Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Gly	Glu	Ile	Ile
305					310					315					320
Gly	Asp	Ile	Arg	Gln	Ala	Tyr	Cys	Ile	Ile	Asn	Lys	Thr	Glu	Trp	Asn
				325					330					335	
Ser	Thr	Leu	Gln	Gly	Val	Ser	Lys	Lys	Leu	Glu	Glu	His	Phe	Ser	Lys
			340					345					350		
Lys	Ala	Ile	Lys	Phe	Glu	Pro	Ser	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr
		355					360					365			
Thr	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asp	Thr	Ser
						375					380				
Gln	Leu	Phe	Asn	Ser	Thr	Tyr	Ser	Pro	Ser	Phe	Asn	Gly	Thr	Glu	Asn
385					390					395					400
Lys	Leu	Asn	Gly	Thr	Ile	Thr	Ile	Thr	Cys	Arg	Ile	Lys	Gln	Ile	Ile
				405					410					415	
Asn	Met	Trp	Gln	Lys	Val	Gly	Arg	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Ala

420					425					430					
Gly	Asn	Leu	Thr	Cys	Glu	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg
		435					440					445			
Asp	Gly	Gly	Lys	Thr	Gly	Pro	Asn	Asp	Thr	Glu	Ile	Phe	Arg	Pro	Gly
	450					455					460				
Gly	Gly	Asp	Met	Arg	Asp	Asn	Trp	Arg	Asn	Glu	Leu	Tyr	Lys	Tyr	Lys
465					470					475					480
Val	Val	Glu	Ile	Lys	Pro	Leu	Gly	Val	Ala	Pro	Thr	Glu	Ala	Lys	Arg
				485					490					495	
Arg	Val	Val	Glu	Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Val	Phe
			500					505					510		
Leu	Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Ala	Ser	Ile
		515					520					525			
Thr	Leu	Thr	Val	Gln	Ala	Arg	Leu	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln
	530					535					540				
Gln	Asn	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Leu	Leu	Gln
545					550					555					560
Leu	Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Thr	Arg	Ile	Leu	Ala	Val
			565						570					575	
Glu	Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser
			580					585					590		
Gly	Lys	Leu	Ile	Cys	Thr	Thr	Ala	Val	Pro	Trp	Asn	Ser	Ser	Trp	Ser
		595					600					605			
Asn	Arg	Ser	His	Asp	Glu	Ile	Trp	Asp	Asn	Met	Thr	Trp	Met	Gln	Trp
		610				615					620				
Asp	Arg	Glu	Ile	Asn	Asn	Tyr	Thr	Asp	Thr	Ile	Tyr	Arg	Leu	Leu	Glu
625					630					635					640
Glu	Ser	Gln	Asn	Gln	Gln	Glu	Lys	Asn	Glu	Lys	Asp	Leu	Leu	Ala	Leu
			645						650					655	
Asp	Ser	Trp	Gln	Asn	Leu	Trp	Asn	Trp	Phe	Ser	Ile	Thr	Asn	Trp	Leu
			660					665					670		
Trp	Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Ile	Gly	Leu
		675					680					685			
Arg	Ile	Ile	Phe	Ala	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Gln	Gly
						695					700				
Tyr	Ser	Pro	Leu	Pro	Phe	Gln	Thr	Leu	Thr	Pro	Asn	Pro	Arg	Glu	Pro
705					710					715					720

Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Gly
 725 730 735
 Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu Ala Trp Asp Asp
 740 745 750
 Leu Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Phe Ile
 755 760 765
 Leu Ile Ala Ala Arg Val Leu Glu Leu Leu Gly Gln Arg Gly Trp Glu
 770 775 780
 Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln Tyr Trp Gly Leu Glu Leu
 785 790 795 800
 Lys Lys Ser Ala Ile Ser Leu Leu Asp Thr Ile Ala Ile Ala Val Ala
 805 810 815
 Glu Gly Thr Asp Arg Ile Ile Glu Phe Ile Gln Arg Ile Cys Arg Ala
 820 825 830
 Ile Arg Asn Ile Pro Arg Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu
 835 840 845

Gln

<210> 24
 <211> 855
 <212> PRT
 <213> Human immunodeficiency virus

<400> 24
 Met Arg Val Arg Gly Ile Leu Arg Ser Trp Gln Gln Trp Trp Ile Trp
 1 5 10 15
 Gly Ile Leu Gly Phe Trp Ile Cys Ser Gly Leu Gly Asn Leu Trp Val
 20 25 30
 Thr Val Tyr Asp Gly Val Pro Val Trp Arg Glu Ala Ser Thr Thr Leu
 35 40 45
 Phe Cys Ala Ser Asp Ala Lys Ala Tyr Glu Lys Glu Val His Asn Val
 50 55 60
 Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro Gln Glu Ile
 65 70 75 80
 Glu Leu Asp Asn Val Thr Glu Asn Phe Asn Met Trp Lys Asn Asp Met
 85 90 95
 Val Asp Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp Gln Ser Leu
 100 105 110
 Lys Pro Arg Val Lys Leu Thr Pro Leu Cys Val Thr Leu Lys Cys Thr

115					120					125					
Asn	Tyr	Ser	Thr	Asn	Tyr	Ser	Asn	Thr	Met	Asn	Ala	Thr	Ser	Tyr	Asn
130						135					140				
Asn	Asn	Thr	Thr	Glu	Glu	Ile	Lys	Asn	Cys	Thr	Phe	Asn	Met	Thr	Thr
145					150					155					160
Glu	Leu	Arg	Asp	Lys	Lys	Gln	Gln	Val	Tyr	Ala	Leu	Phe	Tyr	Lys	Leu
				165					170					175	
Asp	Ile	Val	Pro	Leu	Asn	Ser	Asn	Ser	Ser	Glu	Tyr	Arg	Leu	Ile	Asn
			180					185					190		
Cys	Asn	Thr	Ser	Ala	Ile	Thr	Gln	Ala	Cys	Pro	Lys	Val	Ser	Phe	Asp
		195					200					205			
Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	Pro	Ala	Gly	Tyr	Ala	Ile	Leu	Lys
	210					215					220				
Cys	Lys	Asn	Asn	Thr	Ser	Asn	Gly	Thr	Gly	Pro	Cys	Gln	Asn	Val	Ser
225					230					235					240
Thr	Val	Gln	Cys	Thr	His	Gly	Ile	Lys	Pro	Val	Val	Ser	Thr	Pro	Leu
				245					250					255	
Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	Gly	Gly	Glu	Ile	Ile	Ile	Arg	Ser
			260					265					270		
Lys	Asn	Leu	Ser	Asn	Asn	Ala	Tyr	Thr	Ile	Ile	Val	His	Leu	Asn	Asp
		275					280					285			
Ser	Val	Glu	Ile	Val	Cys	Thr	Arg	Pro	Asn	Asn	Asn	Thr	Arg	Lys	Gly
		290				295					300				
Ile	Arg	Ile	Gly	Pro	Gly	Gln	Thr	Phe	Tyr	Ala	Thr	Glu	Asn	Ile	Ile
305					310					315					320
Gly	Asp	Ile	Arg	Gln	Ala	His	Cys	Asn	Ile	Ser	Ala	Gly	Glu	Trp	Asn
				325				330						335	
Lys	Ala	Val	Gln	Arg	Val	Ser	Ala	Lys	Leu	Arg	Glu	His	Phe	Pro	Asn
			340					345					350		
Lys	Thr	Ile	Glu	Phe	Gln	Pro	Ser	Ser	Gly	Gly	Asp	Leu	Glu	Ile	Thr
		355					360					365			
Thr	His	Ser	Phe	Asn	Cys	Arg	Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Thr	Ser
						375					380				
Lys	Leu	Phe	Asn	Ser	Ser	Tyr	Asn	Gly	Thr	Ser	Tyr	Arg	Gly	Thr	Glu
385					390					395					400
Ser	Asn	Ser	Ser	Ile	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Ile	Ile
				405					410					415	
Asp	Met	Trp	Gln	Lys	Val	Gly	Arg	Ala	Ile	Tyr	Ala	Pro	Pro	Ile	Glu

420					425					430					
Gly	Asn	Ile	Thr	Cys	Ser	Ser	Ser	Ile	Thr	Gly	Leu	Leu	Leu	Ala	Arg
	435						440					445			
Asp	Gly	Gly	Leu	Asp	Asn	Ile	Thr	Thr	Glu	Ile	Phe	Arg	Pro	Gln	Gly
	450					455					460				
Gly	Asp	Met	Lys	Asp	Asn	Trp	Arg	Asn	Glu	Leu	Tyr	Lys	Tyr	Lys	Val
465						470					475				480
Val	Glu	Ile	Lys	Pro	Leu	Gly	Val	Ala	Pro	Thr	Glu	Ala	Lys	Arg	Arg
				485					490					495	
Val	Val	Glu	Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Val	Ile	Phe
			500					505					510		
Gly	Phe	Leu	Gly	Ala	Ala	Gly	Ser	Asn	Met	Gly	Ala	Ala	Ser	Ile	Thr
	515						520					525			
Leu	Thr	Ala	Gln	Ala	Arg	Gln	Leu	Leu	Ser	Gly	Ile	Val	Gln	Gln	Gln
	530					535					540				
Ser	Asn	Leu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Gln	His	Met	Leu	Gln	Leu
545						550					555				560
Thr	Val	Trp	Gly	Ile	Lys	Gln	Leu	Gln	Ala	Arg	Val	Leu	Ala	Ile	Glu
				565					570					575	
Arg	Tyr	Leu	Lys	Asp	Gln	Gln	Leu	Leu	Gly	Ile	Trp	Gly	Cys	Ser	Gly
			580					585					590		
Lys	Leu	Ile	Cys	Thr	Thr	Thr	Val	Pro	Trp	Asn	Ser	Ser	Trp	Ser	Asn
	595						600					605			
Lys	Thr	Gln	Gly	Glu	Ile	Trp	Glu	Asn	Met	Thr	Trp	Met	Gln	Trp	Asp
	610					615					620				
Lys	Glu	Ile	Ser	Asn	Tyr	Thr	Gly	Ile	Ile	Tyr	Arg	Leu	Leu	Glu	Glu
625						630					635				640
Ser	Gln	Asn	Gln	Gln	Glu	Gln	Asn	Glu	Lys	Asp	Leu	Leu	Ala	Leu	Asp
			645					650						655	
Ser	Arg	Asn	Asn	Leu	Trp	Ser	Trp	Phe	Asn	Ile	Ser	Asn	Trp	Leu	Trp
			660					665					670		
Tyr	Ile	Lys	Ile	Phe	Ile	Met	Ile	Val	Gly	Gly	Leu	Ile	Gly	Leu	Arg
	675					680						685			
Ile	Ile	Phe	Ala	Val	Leu	Ser	Ile	Val	Asn	Arg	Val	Arg	Gln	Gly	Tyr
	690					695					700				
Ser	Pro	Leu	Ser	Phe	Gln	Thr	Leu	Thr	Pro	Asn	Pro	Arg	Gly	Leu	Asp
705						710					715				720

Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu Gln Asp Arg Asp Arg
 725 730 735
 Ser Ile Arg Leu Val Gln Gly Phe Leu Ala Leu Ala Trp Asp Asp Leu
 740 745 750
 Arg Ser Leu Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Ile Leu
 755 760 765
 Val Thr Ala Arg Val Val Glu Leu Leu Gly Arg Ser Ser Pro Arg Gly
 770 775 780
 Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu Gly Ser Leu Val Gln
 785 790 795 800
 Tyr Trp Gly Leu Glu Leu Lys Lys Ser Ala Thr Ser Leu Leu Asp Ser
 805 810 815
 Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Val Ile
 820 825 830
 Gln Arg Ile Tyr Arg Ala Phe Cys Asn Ile Pro Arg Arg Val Arg Gln
 835 840 845
 Gly Phe Glu Ala Ala Leu Gln
 850 855

<210> 25
 <211> 20
 <212> PRT
 <213> Human immunodeficiency virus

<400> 25
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 1 5 10 15

Phe Phe Lys Thr
 20

<210> 26
 <211> 60
 <212> DNA
 <213> Human immunodeficiency virus

<400> 26
 gacataaaac aaggaccaa agagcccttt agagactatg tagaccgggt ctttaaaacc 60

<210> 27
 <211> 20
 <212> PRT
 <213> Human immunodeficiency virus

<400> 27
 Asp Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg

1	5	10	15
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Phe Phe Lys Thr
20

<210> 28
 <211> 47
 <212> PRT
 <213> Human immunodeficiency virus

<400> 28
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 Lys Val Gly Arg Ala Met Tyr Ala Pro Pro Ile Ala Gly Asn Leu Thr
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 Cys Glu Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly
 35 40 45

<210> 29
 <211> 48
 <212> PRT
 <213> Human immunodeficiency virus

<400> 29
 Ser Ile Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asp Met Trp
 1 5 10 15
 Gln Lys Val Gly Arg Ala Ile Tyr Ala Pro Pro Ile Glu Gly Asn Ile
 20 25 30
 Thr Cys Ser Ser Ser Ile Thr Gly Leu Leu Leu Ala Arg Asp Gly Gly
 35 40 45

<210> 30
 <211> 4
 <212> PRT
 <213> Human immunodeficiency virus

<400> 30
 Gly Gly Gly Ser